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AMENDMENTS TO THE CLAIMS

Listing of Claims

- 1. (Previously presented) A method for the fermentative production of L-methionine, which comprises the following steps:
 - a) fermenting in a medium cells of coryneform bacterium Corynebacterium glutamicum for producing L-methionine, said coryneform bacteria expressing at least one heterologous nucleotide sequence which sodes for a protein with homoserine O-acetyltransferase (metA) activity, wherein said heterologous nucleotide sequence comprises a nucleotide sequence encoding a metA protein derived from Corynebacterium diphteriae having an amino acid sequence as set forth in SEQ ID NO: 2;
 - b) concentrating L-methionine in the medium or in the bacterial cells, and
 - c) isolating L-methionine.
- 2-4, (Cancelled)
- 5. (Previously presented) The method as claimed in claim 1, wherein the metA-encoding nucleotide sequence comprises a coding sequence as set forth in SEQ ID NO:1.
- 6. (Cancelled)

met A encoding

- 7. (Previously presented) The method as claimed in claim 1, wherein the eoding met A sequence is a DNA or RNA which can be replicated in coryneform bacteria or is stably integrated into the chromosome.
- 8. (Previously presented) The method as claimed in claim 7, wherein
 - a bacteria strain transformed with a plasmid vector carrying at least one copy of the coding metA sequence under the control of regulatory sequences is used, or a strain in which the coding metA sequence has been integrated into the bacterial
 - b) a strain in which the coding metA sequence has been integrated into the bacterial chromosome is used.

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methencoding

- 9. (Previously presented) The method as claimed in claim 1, wherein the coding metA sequence is overexpressed.
- 10. (Currently amended) The method as claimed in claim 1, wherein bacteria are fermented in which additionally at least one further gene of the biosynthetic pathway of L-methionine has been amplified or mutated overexpressed such that its activity is not influenced by metabolic metabolites.
- 11. (Cancelled)
- 12. (Currently amended) The method of claim 1, wherein coryneform bacteria are fermented in which, at the same time, a lysC gene derived from a coryneform bacterium, which encodes an aspartate kinase, is overexpressed or mutated in such a way that the activity of the corresponding protein is influenced by metabolic metabolites to a smaller extent, if at all, compared to a nonmutated protein.
- 13. (Cancelled)

14. (Previously presented) The method of claim 17, wherein the coryneform bacterium is of the species Corynebacterium glutamicum.

15-16. (Cancelled)

- 17. (Currently amended) A method for the production of L-methionine, which comprises the following steps:
 - a) fermenting in a medium cells of a coryneform bacterium for producing Lmethionine, said coryneform bacteria expressing at least one heterologous
 nucleotide sequence which eodes for a protein with homoserine Oacetyltransferase (metA) activity, wherein the heterologous metA encoding
 nucleotide sequence is less than 100% homologous to the metA encoding

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sequence from Corynebacterium glutamieum ATCC 13032 comprises a nucleotide sequence having 95% identity or more to the sequence as set forth in SEO ID NO: 1;

- b) concentrating L-methionine in the medium or in the bacterial cells; and
- c) isolating L-methionine.
- 18. (Previously presented) The method of claim 17, wherein the metA-encoding nucleotide sequence comprises a-coding sequence as set forth in SEQ ID NO:1.
- 19. (Currently amended) The method of claim 17, wherein the metA-encoding nucleotide sequence codes for a protein with metA activity, said protein comprising an amino acid sequence as set forth in SEQ ID NO: 2 or a fragment of SEQ ID NO: 2 having metA activity.
- 20. (Previously presented) The method of claim 17, wherein the eoding metA sequence is a DNA or RNA which can be replicated in coryneform bacteria or is stably integrated into the chromosome.
- 21. (Previously presented) The method of claim 17, wherein
 - a) a bacteria strain transformed with a plasmid vector carrying at least one copy of net A broken the coding metA sequence under the control of regulatory sequences is used, or mut the coding metA sequence has been integrated into the bacterial
 - b) a strain in which the coding metA sequence has been integrated into the bacterial chromosome is used.
- 22. (Previously presented) The method of claim 17, wherein the coding metA sequence is overexpressed.
- 23. (Currently amended) The method of claim 17, wherein bacteria are fermented in which additionally at least one further gene of the biosynthetic pathway of L-methionine has been amplified or mutated overexpressed such that its activity is not influenced by metabolic metabolites.

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- 24. (Currently amended) A method for the production of L-methionine, which comprises the following steps:
 - a) fermenting in a medium cells of a coryneform bacterium for producing of Lmethionine, said coryneform bacteria expressing at least one heterologous
 nucleotide sequence which codes for a protein with homoserine Oacetyltransferase (metA) activity, wherein said heterologous nucleotide sequence
 comprises a nucleotide sequence encoding a metA protein having an amino acid
 sequence with 95% homology or more to the sequence as set forth in SEQ ID NO:
 2 derived from Corynebacterium diphteriae;
 - b) concentrating L-methionine in the medium or in the bacterial cells; and
 - c) isolating L-methionine.

25-26. (Cancelled)

27. (Previously presented) The method of claim 24, wherein the soding metA sequence is a DNA or RNA which can be replicated in coryneform bacteria or is stably integrated into the chromosome.

- 28. (Previously presented) The method of claim 24, wherein
 - a) a bacteria strain transformed with a plasmid vector carrying at least one copy of metal encoding the coding metal sequence under the control of regulatory sequences is used, or metal encoding metals.
 - b) a strain in which the coding mot A sequence has been integrated into the bacterial chromosome is used.
- 29. (Previously presented) The method of claim 24, wherein the coding metA sequence is overexpressed.
- 30. (Currently amended) The method of claim 24, wherein bacteria are fermented in which additionally at least one further gene of the biosynthetic pathway of L-methionine has been amplified or mutated overexpressed such that its activity is not influenced by metabolic metabolites.

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31. (Previously presented) The method of claim 24, wherein the coryneform bacterium is of the species Corynebacterium glutamicum.